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MPSRCH (TM)
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MPsrch_pp on: protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated.

Database: a-geneseq32
Listing first 45 summaries

On: Tue Mar 23 15:01:25 1999; MasPar time 2.89 Seconds
61.491 Million cell updates/sec

Title: >US-08-766-350A-2
Description: (24-34) from US08766350A.pep (2 of 4)
Perfect Score: 63
Sequence: 1 MTQSPSSLSAS 11

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%

Database:
a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 15.144; Variance 52.220; scale 0.290

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	63	100.0	104	29	W52225	Antibody LD2-4-VL cha	3.52e+00
2	63	100.0	105	29	W52217	Antibody LD1-84-VL ch	3.52e+00
3	63	100.0	105	29	W52239	Antibody LD1-6-17-VL	3.52e+00
4	63	100.0	105	29	W52241	Antibody LD1/2-6-3-VL	3.52e+00
5	63	100.0	105	29	W52219	Antibody LD1-110-VL c	3.52e+00
6	63	100.0	105	29	W52237	Antibody LD2-20-VL ch	3.52e+00
7	63	100.0	105	29	W52233	Antibody LD2-14-VL ch	3.52e+00
8	63	100.0	106	29	W52213	Antibody LD1-40-VL ch	3.52e+00
9	63	100.0	106	29	W52215	Antibody LD1-52-VL ch	3.52e+00
10	63	100.0	106	29	W52227	Antibody LD2-5-VL cha	3.52e+00
11	63	100.0	106	29	W52221	Antibody LD1-117-VL c	3.52e+00
12	63	100.0	106	24	W22412	Humanised alpha-4 int	3.52e+00
13	63	100.0	107	29	W41390	Anti-CEA antibody lig	3.52e+00
14	63	100.0	107	29	W41397	Anti-CEA antibody 806	3.52e+00
15	63	100.0	107	29	W23953	Chimeric humanised Mu	3.52e+00
16	63	100.0	107	29	W44123	Light chain variable	3.52e+00
17	63	100.0	107	27	W27568	Anti-TNF-alpha antibo	3.52e+00
18	63	100.0	107	21	W11920	Humanised MAb SK48-E2	3.52e+00
19	63	100.0	107	14	R79247	Light chain variable	3.52e-00
20	63	100.0	107	14	R78972	Light chain variable	3.52e-00
21	63	100.0	108	27	W23440	Modified light chain	3.52e+00
22	63	100.0	108	27	W23439	Modified light chain	3.52e+00
23	63	100.0	108	28	W23442	hWI2 light chain.	3.52e+00
24	63	100.0	108	21	W04177	Variant variable ligh	3.52e+00
25	63	100.0	108	5	R28751	Light chain variable	3.52e+00
26	63	100.0	113	29	W42472	Interleukin-5 humanis	3.52e+00
27	63	100.0	117	28	W41147	Human vkappa65.15 fra	3.52e+00
28	63	100.0	126	28	W23954	Humanised light chain	3.52e+00
29	63	100.0	126	14	R76678	Human/murine chimeric	3.52e+00
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31	63	100.0	126	14	R76675	Human/murine chimeric	3.52e+00
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33	63	100.0	126	19	R76680	Human/murine chimeric	3.52e+00
34	63	100.0	126	27	W04388	Chimeric human/murin	3.52e+00
35	63	100.0	128	27	W31691	Humanised anti-VLA-4	3.52e+00
36	63	100.0	128	18	R90684	Humanised 5C7.29 anti	3.52e+00
37	63	100.0	214	26	W34504	Light chain of humani	3.52e+00
38	63	100.0	214	26	W34506	Light chain of full l	3.52e+00
39	63	100.0	234	21	W11638	Human anti-RSV monocl	3.52e+00
40	63	100.0	235	29	W41411	Humanised light chain	3.52e+00
41	63	100.0	235	29	W41398	Humanised antibody 80	3.52e+00
42	63	100.0	235	21	W11640	Human anti-RSV monocl	3.52e+00
43	63	100.0	240	29	W23954	Chimeric humanised Mu	3.52e+00
44	63	100.0	245	19	R98943	Humanised anti-CD38 m	3.52e+00
45	63	100.0	355	28	W35133	R. Pipiens recombinan	3.52e+00

ALIGNMENTS

RESULT 1

```
ID   W52225 standard; Protein; 104 AA.
AC   W52225;
DT   12-JUN-1998  (first entry)
DE   Antibody LD2-4-VL chain sequence.
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
OS   Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1997; EP-810421.
PR   24-JUN-1996; EP-03253.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
PI   WPI; 98-077173/07.
DR   N-PSDB; V19749.
PT   New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT   Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
PS   Claim 1; Fig 7B; 68pp; English.
CC   This sequence is the antibody LD2-4-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative women before or immediately after the birth
CC   of a Rhesus positive child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence   104 AA.

Query Match             100.0%;  Score 63;  DB 29;  Length 104;
Best Local Similarity   100.0%;  Pred. No. 3.52e+00;
Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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PD   31-DEC-1997.
PF   20-JUN-1997; E03253.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   WPI; 98-077173/07.
DR   N-PSDB; V19745.
PT   New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT   Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura.
PS   Claim 1; Fig 5B; 68pp; English.
CC   This sequence is the antibody LD1-117-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 106 AA.

Query Match   100.0%;   Score 63;   DB 29;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 3.52e+00;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   2 mtgspsslsas 12
        |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 12
ID   W22412 standard; Protein; 106 AA.
AC   W22412;
DT   08-DEC-1997 (first entry)
DE   Humanised alpha-4 integrin antibody 21.6 VL La.
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
FH   Key   Location/Qualifiers
FH
FT   region   1..23
FT   /label= FR1
FT   region   24..34
FT   /note= "REI framework region 1"
FT   /label= CDR1
FT   region   35..49
FT   /note= "21.6 complementarity determining region 1"
FT   /label= FR2
FT   misc_difference 45
FT   /note= "REI framework region 2"
FT   /note= "REI Lys-45 is substd. by Lys of mouse
FT   21.6 VL, important in supporting the
FT   CDR2 loop."
FT   /label= CDR2
FT   region   49
FT   /note= "21.6 complementarity determining region 2"
FT   misc_difference 49
FT   /label= FR3
FT   /note= "REI Tyr-49 is substd. by His of mouse
FT   21.6 VL, located at the binding site"
FT   region   50..56
FT   /note= "REI Lys-45 is substd. by Lys of mouse
FT   21.6 VL, important in supporting the
FT   /label= CDR2

FT   /note= "REI framework region 3"
FT   misc_difference 58
FT   /note= "REI Val-58 is substd. by Ile of mouse
FT   21.6 VL, involved in antibody-antigen
FT   binding"
FT   /note= "21.6 VL, important in supporting the CDR2
FT   region   69   loop"
FT   /note= "REI Thr-69 is substd. by Arg of mouse
FT   21.6 VL, involved in antibody-antigen
FT   binding"
FT   /label= FR4
FT   region   97..106
FT   /note= "21.6 complementarity determining region 3"
FT   /label= CDR3
FT   misc_difference 103
FT   /note= "REI framework region 4"
FT   /note= "REI Leu-103 substd. by Val, more typical
FT   of human kappa light chain J region."
FT   misc_difference 104
FT   /note= "REI Gln-104 substd. by Glu, more typical
FT   of human kappa light chain J region."
FT   misc_difference 106
FT   /note= "REI Thr-106 substd. by Lys, more typical
FT   of human kappa light chain J region"

misc_difference 69
                /note= "REI framework region 3"
misc_difference 58
                /note= "21.6 VL, Important in supporting the CDR2
                loop"

Query Match   100.0%;   Score 63;   DB 24;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 3.52e+00;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   4 mtgspsslsas 14
        |||||||||||
Qy   24 MTQSPSSLSAS 34

PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
PS   Claim 25; Fig 6; 107pp; English.
DR   WPI; 97-297879/27.
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
PR   21-NOV-1995; US-561521.
PF   21-NOV-1995; U18807.
PD   29-MAY-1997.
PN   WO9718838-A1.
FT   of human kappa light chain J region.
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see W22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework. It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see W22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
SQ   Sequence 106 AA.

RESULT 13
ID   W41390 standard; Protein; 107 AA.
AC   W41390;
DT   02-JUN-1998 (first entry)
DE   Anti-CEA antibody light chain variable region VK4.
KW   Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW   cancer diagnosis; complementarity determining region; light chain.
OS   Synthetic.
PN   WO9742329-A1.

MPSRCH (TM)

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**********************************************************
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

on: Tue Mar 23 15:20:39 1999; MasPar time 1.37 Seconds
                                34.477 Million cell updates/sec

Tabular output not generated.

Title:	
Description:	>US-08-766-350A-4
Perfect Score:	31
Sequence:	(31-35) from US08766350A.pep (2 of 4)
	1 VRSGA 5
Scoring table:	PAM 150
	Gap 11
Searched:	100342 seqs, 9469514 residues
Database:	a-issued
	Listing first 45 summaries
	1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1
Post-processing:	Minimum Match 0%
Searched:	
Statistics:	Mean 11.797; Variance 23.980; scale 0.492

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	31	100.0	124	2	US-08-471-	Sequence 6, Applicati	1.86e+02
2	31	100.0	124	1	US-08-017-	Sequence 4, Applicatio	1.86e+02
3	31	100.0	124	1	US-08-471-	Sequence 6, Applicatio	1.86e+02
4	31	100.0	124	3	PCT-US94-0	Sequence 6, Applicatio	1.86e+02
5	31	100.0	124	1	US-08-017-	Sequence 6, Applicatio	1.86e+02
6	31	100.0	124	3	PCT-US94-0	Sequence 4, Applicatio	1.86e+02
7	31	100.0	221	1	US-08-542-	Sequence 5, Applicati	1.86e+02
8	31	100.0	341	1	US-08-314-	Sequence 19, Applicati	1.86e+02
9	31	100.0	386	2	US-08-663-	Sequence 6, Applicati	1.86e+02
10	31	100.0	484	1	US-08-482-	Sequence 26, Applicati	1.86e+02
11	31	100.0	484	1	US-08-127-	Sequence 26, Applicati	1.86e+02
12	31	100.0	659	1	US-08-136-	Sequence 3, Applicatio	1.86e+02
13	31	100.0	659	1	US-08-479-	Sequence 3, Applicatio	1.86e+02
14	31	100.0	691	3	PCT-US91-0	Sequence 2, Applicatio	1.86e+02
15	29	93.5	185	4	5514590-10	Sequence 7, Applicatio	3.70e+02
16	29	93.5	185	2	US-08-379-	Sequence 14, Applicati	3.70e+02
17	29	93.5	185	1	US-08-278-	Patent No. 5514590.	3.70e+02
18	29	93.5	185	1	US-08-483-	Sequence 14, Applicati	3.70e+02
19	29	93.5	185	2	US-08-472-	Sequence 14, Applicati	3.70e+02
20	29	93.5	185	2	US-08-487-	Sequence 14, Applicati	3.70e+02
21	29	93.5	299	4	5514590-4	Patent No. 5514590.	3.70e+02
22	29	93.5	396	2	US-08-926-	Sequence 2, Applicatio	3.70e+02
23	29	93.5	421	2	US-07-955-	Sequence 27, Applicati	3.70e+02
24	29	93.5	471	3	PCT-US95-0	Sequence 2, Applicatio	3.70e+02
25	29	93.5	516	1	US-08-356-	Sequence 4, Applicatio	3.70e+02
26	29	93.5	553	2	US-08-561-	Sequence 16, Applicati	3.70e+02
27	29	93.5	559	2	US-08-406-	Sequence 20, Applicati	3.70e+02
28	29	93.5	1018	2	US-08-714-	Sequence 6, Applicatio	3.70e+02
29	29	93.5	1018	2	US-08-452-	Sequence 2, Applicatio	3.70e+02
30	29	93.5	1018	1	US-08-408-	Sequence 6, Applicatio	3.70e+02
31	29	93.5	1018	1	US-08-408-	Sequence 6, Applicatio	3.70e+02
32	29	93.5	1045	1	US-07-783-	Sequence 6, Applicatio	3.70e+02
33	29	93.5	1045	1	US-07-934-	Sequence 6, Applicatio	3.70e+02
34	29	93.5	1045	1	US-07-596-	Sequence 6, Applicatio	3.70e+02
35	29	90.3	275	4	5472855-4	Patent No. 5472855.	5.19e+02
36	28	90.3	380	1	RE34606-2	Patent No. RE34,606.	5.19e+02
37	28	90.3	616	2	US-08-638-	Sequence 35, Applicati	5.19e+02
38	28	90.3	774	1	US-07-747-	Sequence 3, Applicati	5.19e+02
39	28	90.3	774	1	US-08-019-	Sequence 5, Applicati	5.19e+02
40	28	90.3	780	1	US-08-786-	Sequence 14, Applicati	5.19e+02
41	28	90.3	853	2	US-08-638-	Sequence 27, Applicati	5.19e+02
42	28	90.3	853	1	US-08-638-	Sequence 31, Applicati	5.19e+02
43	28	90.3	1958	1	US-07-945-	Sequence 2, Applicatio	5.19e+02
44	28	90.3	2842	1	US-08-289-	Sequence 7, Applicatio	5.19e+02
45	28	90.3	2873	2	US-08-638-	Sequence 2, Applicatio	5.19e+02

ALIGNMENTS

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ID   US-08-471-426-6      STANDARD;      PRT;     124 AA.
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AC   xxxxxx
XX
DT
DE
XX
XX   xxxxxx

Sequence 6, Application US/08471426

Patent No. 5808033
Sequence 6, Application US/08471426
GENERAL INFORMATION:
   APPLICANT: GOURLIE, BRIAN B
   APPLICANT: RIXON, MARK W
   APPLICANT: MEZES, PETER S
   APPLICANT: KAPLAN, DONALD A
   APPLICANT: SCHLOM, JEFFREY
   TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
   TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
   NUMBER OF SEQUENCES: 24
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Duane C. Ulmer
      STREET: P.O. Box 1967
      CITY: Midland
      STATE: MI
      COUNTRY: US
      ZIP: 48641-1967
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/471,426
      FILING DATE: 06-JUN-1995
      CLASSIFICATION: 536
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/017,570
      FILING DATE: 16-FEB-1993
   ATTORNEY/AGENT INFORMATION:
      NAME: ULMER, DUANE C
      REGISTRATION NUMBER: 34,941
      REFERENCE/DOCKET NUMBER: C-38,777
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
   SEQUENCE CHARACTERISTICS:
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CC      LENGTH:    124 amino acids
CC      TYPE:      amino acid
CC      TOPOLOGY:  linear
SO      MOLECULE TYPE:  protein
SQ      SEQUENCE  124 AA; 13816 MW; 93186 CN;

Qy      31  VRSGA 35
Db      12  VRSGA 16
        |||||
        31  VRSGA 35

Matches       5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
Best Local Similarity 100.0%;  Pred. No. 1.86e+02;
Query Match                    100.0%;  Score 31;  DB 2;  Length 124;

RESULT    2
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XX
DE      xxxxxx
XX
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    Patent No. 5472693
    GENERAL INFORMATION:
CC      APPLICANT:  GOURLIE, BRIAN B
CC      APPLICANT:  RIXON, MARK W
CC      APPLICANT:  MEZES, PETER S
CC      APPLICANT:  KAPLAN, DONALD A
CC      APPLICANT:  SCHLOM, JEFFREY
CC      TITLE OF INVENTION:  A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
CC      TITLE OF INVENTION:  ANTIGEN CHIMERIC ANTIBODIES
CC      NUMBER OF SEQUENCES:    24
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE:  Duane C. Ulmer
CC      STREET:  P. O. Box 1967
CC      CITY:  Midland
CC      STATE:  MI
CC      COUNTRY:  US
CC      ZIP:  48641-1967
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE:  Floppy disk
CC      COMPUTER:  IBM PC compatible
CC      OPERATING SYSTEM:  PC-DOS/MS-DOS
CC      SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER:  US/08/017,570
CC      FILING DATE:  19930216
CC      CLASSIFICATION:  424
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME:  ULMER, DUANE C
CC      REGISTRATION NUMBER:  34,941
CC      REFERENCE/DOCKET NUMBER:  C-38,777
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE:  (517) 636-8104
CC      INFORMATION FOR SEQ ID NO:  4:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH:  124 amino acids
CC      TYPE:  AMINO ACID
CC      TOPOLOGY:  linear
CC      MOLECULE TYPE:  protein
SQ      SEQUENCE  124 AA; 13786 MW; 91250 CN;
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AC
XX
DT
XX
DE      xxxxxx
XX
    Sequence 4, Application US/08471426
    Patent No. 5808033
    GENERAL INFORMATION:
CC      APPLICANT:  GOURLIE, BRIAN B
CC      APPLICANT:  RIXON, MARK W
CC      APPLICANT:  MEZES, PETER S
CC      APPLICANT:  KAPLAN, DONALD A
CC      APPLICANT:  SCHLOM, JEFFREY
CC      TITLE OF INVENTION:  A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
CC      TITLE OF INVENTION:  ANTIGEN CHIMERIC ANTIBODIES
CC      NUMBER OF SEQUENCES:    24
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE:  Duane C. Ulmer
CC      STREET:  P. O. Box 1967
CC      CITY:  Midland
CC      STATE:  MI
CC      COUNTRY:  US
CC      ZIP:  48641-1967
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE:  Floppy disk
CC      COMPUTER:  IBM PC compatible
CC      OPERATING SYSTEM:  PC-DOS/MS-DOS
CC      SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER:  US/08/471,426
CC      FILING DATE:  06-JUN-1995
CC      CLASSIFICATION:  536
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:  08/017,570
CC      FILING DATE:  16-FEB-1993
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME:  ULMER, DUANE C
CC      REGISTRATION NUMBER:  34,941
CC      REFERENCE/DOCKET NUMBER:  C-38,777
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE:  (517) 636-8104
CC      INFORMATION FOR SEQ ID NO:  4:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH:  124 amino acids
CC      TYPE:  amino acid
CC      TOPOLOGY:  linear
CC      MOLECULE TYPE:  protein
SQ      SEQUENCE  124 AA; 13786 MW; 91250 CN;

Qy      31  VRSGA 35
Db      12  VRSGA 16
        |||||
        31  VRSGA 35

Matches       5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
Best Local Similarity 100.0%;  Pred. No. 1.86e+02;
Query Match                    100.0%;  Score 31;  DB 2;  Length 124;

RESULT    4
ID  PCT-US94-01709-6            STANDARD;          PRT;    124 AA.
XX
AC
XX
DT
XX
DE      xxxxxx
XX
    Sequence 6, Application PCT/US9401709
    Sequence 6, Application PCT/US9401709
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